

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:09:10 ; Search time 8498.8 seconds
(without alignments)
30.345 Million cell updates/sec

Title: US-09-851-670-3
Perfect score: 24
Sequence: 1 tggctgctgctgctgctgctgcaag 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

111874

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_estlin:*
3: em_estlin:*
4: em_estlin:*
5: em_estlin:*
6: em_estlin:*
7: em_estlin:*
8: em_estlin:*
9: em_estlin:*
10: em_estlin:*
11: em_estlin:*
12: em_estlin:*
13: em_estlin:*
14: em_estlin:*
15: em_estlin:*
16: em_estlin:*
17: em_estlin:*
18: em_estlin:*
19: em_estlin:*
20: em_estlin:*
21: em_estlin:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	62.5	59	11	BG237930
2	14	58.3	49	11	BG237930
3	14	58.3	49	11	BG237930
4	13.6	56.7	45	13	AZ314853
5	13.6	56.7	45	13	AZ314853
6	13.4	55.8	43	10	AA482116
7	13.4	55.8	46	13	AZ448066
8	13.4	55.8	50	10	AU102540
9	13.4	55.8	50	10	AU104358
10	13.4	55.8	53	10	AA413642
11	13.4	55.8	56	13	AZ445458
12	13.2	55.0	33	13	AZ341288

C 13	13.2	55.0	34	13	CNS00EXA	AL069767	Drosophila
C 14	13	54.2	42	13	AZ350538	AZ350538	1M0088E08
C 15	13	54.2	43	13	AZ349062	AZ349062	1M0088E08
C 16	13	54.2	52	10	AA209172	AA209172	Z64A03.T
C 17	12.8	53.3	46	11	A1790825	A1790825	YK28d11.Y
C 18	12.8	53.3	49	11	H84362	H84362	YK28d11.Y
C 19	12.8	53.3	50	10	AU102537	AU102537	YK28d11.Y
C 20	12.8	53.3	50	10	AU102538	AU102538	YK28d11.Y
C 21	12.8	53.3	50	10	AU102539	AU102539	YK28d11.Y
C 22	12.8	53.3	50	10	AU102540	AU102540	YK28d11.Y
C 23	12.8	53.3	50	10	AU102541	AU102541	YK28d11.Y
C 24	12.8	53.3	50	10	AU102542	AU102542	YK28d11.Y
C 25	12.8	53.3	50	10	AU102543	AU102543	YK28d11.Y
C 26	12.8	53.3	50	10	AU102544	AU102544	YK28d11.Y
C 27	12.8	53.3	50	10	AU102545	AU102545	YK28d11.Y
C 28	12.8	53.3	50	10	AU102546	AU102546	YK28d11.Y
C 29	12.8	53.3	50	10	AU102547	AU102547	YK28d11.Y
C 30	12.8	53.3	50	10	AU102548	AU102548	YK28d11.Y
C 31	12.8	53.3	50	10	AU102549	AU102549	YK28d11.Y
C 32	12.8	53.3	50	10	AU102550	AU102550	YK28d11.Y
C 33	12.8	53.3	50	10	AU102551	AU102551	YK28d11.Y
C 34	12.8	53.3	50	10	AU102552	AU102552	YK28d11.Y
C 35	12.8	53.3	50	10	AU102553	AU102553	YK28d11.Y
C 36	12.8	53.3	50	10	AU102554	AU102554	YK28d11.Y
C 37	12.8	53.3	50	10	AU102555	AU102555	YK28d11.Y
C 38	12.8	53.3	50	10	AU102556	AU102556	YK28d11.Y
C 39	12.8	53.3	50	10	AU102557	AU102557	YK28d11.Y
C 40	12.8	53.3	50	10	AU102558	AU102558	YK28d11.Y
C 41	12.8	53.3	50	10	AU102559	AU102559	YK28d11.Y
C 42	12.8	53.3	50	10	AU102560	AU102560	YK28d11.Y
C 43	12.8	53.3	50	10	AU102561	AU102561	YK28d11.Y
C 44	12.8	53.3	50	10	AU102562	AU102562	YK28d11.Y
C 45	12.8	53.3	50	10	AU102563	AU102563	YK28d11.Y

ALIGNMENTS

RESULT 1
LOCUS BG237930 59 bp mRNA EST 13-FEB-2001
DEFINITION sab09d06.y1 Gm-cl071 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl071-948 5', mRNA sequence.
ACCESSION BG237930
VERSION BG237930.1 GI:12773003
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

1 (bases 1 to 59)
Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corvett, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R. and Wilson, R.

TITLE

Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estevats@wustl.edu

COMMENT

This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com

BASE COUNT	8 a	18 c	30 g	3 t
ORIGIN	Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"			

Query Match	58.3%;	Score 14;	DB 10;	Length 59;
Best Local Similarity	77.3%;	Pred. NO. 5.5e+04;		
Matches 17; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

QY 2 ggcgtgtctggatgtcgaag 23
||| | | | | | | |
Db 37 GGGCCGGCCGGATGGCCGAC 58

RESULT	4
AZ314853/c	
LOCUS	AZ314853
DEFINITION	45 bp DNA
ACCESSION	M00031A19R Mouse 10kb plasmid UNGC1M library Mus musculus genomic
VERSION	AZ314853
KEYWORDS	clone UNGC1M0031A19 R. DNA sequence.
SOURCE	AZ314853.1 GI:10361143
	GSS.
	house mouse.

REFERENCE
AUTHORS

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: A column: 19
Seq primer: CACACAGGAAACACTATGACC
Class: plasmid ends
High quality sequence stop: 45.

FEATURES
source

1. .45
/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="UGGCM0031A19"
/clone_lip="Mouse 10kb plasmid UGGCM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD4strv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnars/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (gii47321149bA129072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	56.78;	Score 13.6;	DB 13;	Length 45;
Best Local Similarity	80.08;	Pred. No. 7.9e+04;		
Matches 16; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

```

QY      1  tgcctgctctgagatgctcg  20
          ||| | | | | | | | | |
Db      23  TGGTTTGTGTGGGATGTGGC   4

```

RESULT	5
AU103055/c	
LOCUS	50 bp mRNA EST 05-APR-2001
DEFINITION	AU103055 Sgugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION	R8C00293 mRNA sequence.
VERSION	AU103055 AU103055.1 GI:13552576
KEYWORDS	EST.
SOURCE	human.

REFERENCE
AUTHORS

TITLE	Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
JOURNAL	Unpublished (2001)
COMMENT	Contact: Yutaka Suzuki

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yszuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. *Gene* 200 (1-2), 149-156 (1997).

FEATURES

```

SOURCE      1. .50
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="HEC00293"
             /clone_lib="Sugano Homo sapiens CDNA library"
BASE COUNT  7 a      25 c      12 g      6 t
ORIGIN

```

Query Match	56.78;	Score 13.6;	DB 10;	Length 50;
Best Local Similarity	80.08;	Pred. No. 7.9e+04;		
Matches 16;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

QY 5 tggctctgagatgtcgaag 24
||||| ||||| |||||
Db 41 TGGTCCGGGAGATGGAAG 22

RESULT	6	
LOCUS	AA482116/c	
DEFINITION	AA482116 43 bp mRNA	EST 08-AUG-1997
ACCESSION	AA482116	
VERSION	2V43C12.s1	Soares ovary tumor NBH07 Homo sapiens cDNA clone
KEYWORDS	IMAGC:756406 3' similar to SW-RI3A_MOUSE P19253 60S RIBOSOMAL PROTEIN L13A ; , mRNA sequence.	
SOURCE	AA482116	
	GI:2209794	
	EST.	
	human.	

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Stepien, M., Tan, F., Theising, B., White, Y., Wylie,
T., Waterston, R., and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
CONTACT: Wilson R
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
TRACE considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..43
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:756406"
/clone_lib="Soares ovary tumor NBHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACATCTGAGAGGAGGAGCGCGGCTTTTCTTTTCTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

BASE COUNT 9 a 13 c 11 g 10 t
ORIGIN

Query Match 55.8%; Score 13.4; DB 10; Length 43;
Best Local Similarity 73.9%; Pred. No. 9.4e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ggctggtctggagatcggaag 24
||||| ||||| | | |||||
DB 38 GGCTGCTCTGGAACCTCTCAAG 16

RESULT 7
LOCUS AZ448066 46 bp DNA GSS 04-OCT-2000
DEFINITION IM0245106r Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0245106 R, DNA sequence.
ACCESSION AZ448066
VERSION AZ448066.1 GI:10600489
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 46)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0245 row: 1 column: 06
Seq primer: CACACAGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers
1..46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0245106"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (p114732114[9b]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 7 a 4 c 23 g 12 t
ORIGIN

Query Match 55.8%; Score 13.4; DB 13; Length 46;
Best Local Similarity 73.9%; Pred. No. 9.5e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ggctggtctggagatcggaag 24
||||| ||||| | | |||||
DB 14 GGCTGGGTGGGTGGGTGGGAGC 36

RESULT 8
LOCUS AU102540 50 bp mRNA EST 05-APR-2001
DEFINITION AU102540 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC05567, mRNA sequence.
ACCESSION AU102540
VERSION AU102540.1 GI:13552061
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki, Y., Tanouda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata,
H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo,
K., Suyama, A., and Sugano, S.
Fine structural analysis of transcription start sites of human
mRNAs using full-length enriched and 5'-end enriched cDNA libraries
Unpublished (2001)

COMMENT

Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
 S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Location/Qualifiers
 1..50

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HRC05567"

/clone_lib="Sugano Homo sapiens cDNA library"

BASE COUNT

7 a 11 c 25 g 7 t

ORIGIN

Query Match 55.8%; Score 13.4; DB 10; Length 50;
 Best Local Similarity 73.9%; Pred. No. 9.5e+04;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY

2 tgctgctggagatgctggaag 24
 ||| || ||||| ||| ||
 Db 19 GGCAGGTTGGCATGCGCGCTG 41

RESULT 9

AU104358 50 bp mRNA EST 05-APR-2001
 LOCUS AU104358 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION HBMA260082, mRNA sequence.

ACCESSION AU104358
 VERSION AU104358.1 GI:13553879
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
 H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
 K., Suyama,A. and Sugano,S.
 Fine structural analysis of transcription start sites of human

TITLE

mRNAs using full-length enriched and 5'-end enriched cDNA libraries
 Unpublished (2001)

JOURNAL

Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

COMMENT

Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
 S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Location/Qualifiers
 1..50

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HBMA260082"

/clone_lib="Sugano Homo sapiens cDNA library"

BASE COUNT

8 a 6 c 26 g 6 t 2 others

ORIGIN

Query Match 55.8%; Score 13.4; DB 10; Length 50;
 Best Local Similarity 70.8%; Pred. No. 9.5e+04;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY

1 tggctgctggagatgctggaag 24
 ||| ||||| ||| ||
 Db 26 TGGCNGTGGGGGCTGCTGGG 49

RESULT 10

AA413642

LOCUS AA413642 53 bp mRNA EST 04-AUG-1997
 DEFINITION vc57b03.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
 IMAGE:778637 5' similar to gb:U16580 Mouse mRNA for
 peptidylarginine deaminase, complete cds (MOUSE);, mRNA sequence.

ACCESSION AA413642
 VERSION AA413642.1 GI:2073779
 KEYWORDS EST.

SOURCE

house mouse.
 Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murine; Mus.

REFERENCE

1 (bases 1 to 53)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

AUTHORS

The WashU-HMI Mouse EST Project
 Unpublished (1996)

TITLE

Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

COMMENT

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:471493

Seq primer: -40ml3 fwd, EF from Amersham.
 Location/Qualifiers
 1..53

FEATURES

source

/organism="Mus musculus"
 /strain="B6D2 F1/J"
 /db_xref="taxon:10090"

ORIGIN

/clone="IMAGE:778637"
 /clone_lib="Knowles Solter mouse 2 cell"
 /tissue_type="embryo"
 /dev_stage="2-cell"
 /lab_host="DH10B"

TITLE

/note="Organ: embryo; Vector: Bluescribe (modified);
 Site:1: MluI; Site:2: SalI; Cloned unidirectionally from
 mRNA prepared from 13,500 2-cell stage embryos. Primer:
 SalI(dT): 5'-CGGTCACCGTCGACCGTCTTTTCTTTT-3'.
 were cloned into the MluI/SalI sites of a modified
 pBluescribe vector using commercial linkers (NEB).
 Average insert size: 1.2 kb."

JOURNAL

Unpublished (1996)

COMMENT

Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

BASE COUNT

10 a 12 c 15 g 16 t

ORIGIN

Query Match 55.8%; Score 13.4; DB 10; Length 53;
 Best Local Similarity 73.9%; Pred. No. 9.5e+04;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY

1 tggctgctggagatgctggaag 23
 ||| ||||| ||||| |||
 Db 29 TGCCTCTCTCTGCTGTCTGANG 51

RESULT 11

A2445458/C

LOCUS A2445458 56 bp DNA GSS 04-OCT-2000
 DEFINITION IM0241J14F mouse 10kb plasmid U06C1M library Mus musculus genomic
 clone U06C1M0241J14 F, DNA sequence.

ACCESSION

A2445458
 VERSION A2445458.1 GI:10595300
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

ORIGIN

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
AUTHORS	1 (bases 1 to 56)	
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Haml,C.,	
	Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly	
	,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.	
	and Wright,D., Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb	
JOURNAL	plasmid inserts	
COMMENT	Unpublished (2000)	
	Contact: Robert B. Weiss	
	University of Utah Genome Center	
	Km. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT	
	84112, USA	
	Tel.: 801 585 5606	
	Fax: 801 585 7177	
	Email: ddunn@genetics.utah.edu	
	Insert length: 10000 Std Error: 0.00	
	Plate: 0241 row: J column: 14	
	Seq primer: CGTGTAAACGACGCCACGT	
	Class: plasmid ends	
	High quality sequence stop: 56.	
FEATURES	Location/Qualifiers	
SOURCE	1..56	
	/organism="Mus musculus"	
	/strain="C57BL/6J"	
	/db_xref="taxon:10090"	
	/clone="UUGC1M0241J14"	
	/clone_lib="Mouse 10kb plasmid UUGC1M library"	
	/sex="Male"	
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"	
	/note="Vector: PWD42nv; Purified genomic DNA from M.	
	musculus C57BL/6J (male) was obtained from the Jackson	
	Laboratory Mouse DNA Resource	
	(http://www.jax.org/resources/documents/dnares/). The DNA	
	was hydrodynamically sheared by repeated passage through a	
	0.005 inch orifice at constant velocity. The sheared DNA	
	was blunt end-repaired with T4 DNA polymerase and T4	
	polynucleotide kinase. Adaptor oligonucleotides were	
	ligated to the blunt ends in high molar excess. The	
	adapted DNA was purified and size-selected for a 9.5 to	
	10.5 kb range using preparative agarose gel	
	electrophoresis. Vector DNA was prepared from a derivative	
	of pMD42 (g14732114[gb AF129072.1]), a copy-number	
	inducible derivative of plasmid RL. The vector was ligated	
	with adaptors complementary to the insert adaptors and	
	purified. The sheared, adapted mouse DNA was annealed to	
	adapted vector DNA, and transformed into	
	chemically-competent E. coli XL10-Gold (Stratagene) cells	
	and selected for ampicillin resistance."	
BASE COUNT	16 a 23 c 2 g 15 t	
ORIGIN		
Query Match	55.8%; Score 13.4; DB 13; Length 56;	
Best Local Similarity	73.9%; Pred. No. 9.5e+04;	
Matches 17; Conservative	0; Mismatches 6; Indels 0; Gaps 0;	
OY	2 ggcgtgctggagatcgctggaagg 24	
Db	37 GATTGATTGATGAGAGAGG 15	
RESULT 12		
LOCUS	AZ341288 33 bp DNA GSS 29-SEP-2000	
DEFINITION	1M0073P05R Mouse 10 kb plasmid UUGC1M library Mus musculus genomic	
ACCESSION	AZ341288	
VERSION	AZ341288.1 GI:10417390	
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus. 1 (bases 1 to 33)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islami,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0073 row: P column: 05 Seq primer: CACACAGCAACACACATGAGCC Class: plasmid ends High quality sequence stop: 33.
FEATURES	location/qualifiers 1..33 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0073P05" /clone_lib="mouse 10kb plasmid UUGC1M library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adpoted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gb AF129072.1]), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adpoted mouse DNA was annealed to adpoted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	7 a 1 c 14 g 11 t
ORIGIN	
Query Match	55.0%; Score 13.2; DB 13; Length 33;
Best Local Similarity	83.3%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY 2 ggcctgctctggatgctgcg 19 	
Db 7 GGCCTGGTGTAGCATGTTG 24	
RESULT 13	
CNS00EXA/c	34 bp DNA GSS 04-JUN-1999
LOCUS	Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION	BACR29D20 of RCI1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL069767
VERSION	AL069767.1
KEYWORDS	GI:4949926

SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 34)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammaster in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp. The same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
source
1. .34
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29D20"
/note="end : TET3"
Location/Qualifiers
BASE COUNT 6 a 18 c 4 g 0 t 6 others
ORIGIN
Query Match 55.0% Score 13.2; DB 13; Length 34;
Best Local Similarity 78.9% Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 tgctggtctggtgcatcgc 19
||| ||| ||| ||| ||| |||
Db 21 TGGGGGCTCGCGGNTGTGC 3
RESULT 14
AZ350538 33 bp DNA GSS 29-SEP-2000
LOCUS AZ350538
DEFINITION IM0088E08F Mouse 10kb plasmid UNGC1M library Mus musculus genomic
clone UNGC1M0088E08 F, DNA sequence.
ACCESSION AZ350538
VERSION AZ350538.1 GI:10429775
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 33)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0088 row: E column: 08
Seq Primer: CGTTGTAAACGACGGCCACT
Class: plasmid ends
High quality sequence stop: 33.
FEATURES
source
1. .33
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10990"
/clone="UNG1M0088E08"
/clone_lib="UNG1M0088E08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g1147321149b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT 5 a 14 c 13 t
ORIGIN
Query Match 54.2% Score 13; DB 13; Length 33;
Best Local Similarity 76.2% Pred. No. 1.3e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 ggcgtgctggatgcgaa 22
||| ||| ||| ||| ||| |||
Db 23 GGATGCTCGGAGGGGAAA 3
RESULT 15
AZ349062 42 bp DNA GSS 29-SEP-2000
LOCUS AZ349062
DEFINITION IM0085H22R Mouse 10kb plasmid UNGC1M library Mus musculus genomic
clone UNGC1M0085H22 R, DNA sequence.
ACCESSION AZ349062
VERSION AZ349062.1 GI:10428299
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 42)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0085 row: H column: 22
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 42.

FEATURES
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1. 42
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0085H22"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

9 a 16 c 4 g 13 t

Query Match 54.2%; Score 13; DB 13; Length 42;
 Best Local Similarity 76.2%; Pred. 1.4e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0;
 QY 1 tggctggtctggagatcgga 21
 ||| |||| ||| |||| ||
 Db 28 TGGTTGATGATGATGATGAGA 8

Search completed: March 9, 2002, 00:09:11
 Job time: 11027 sec